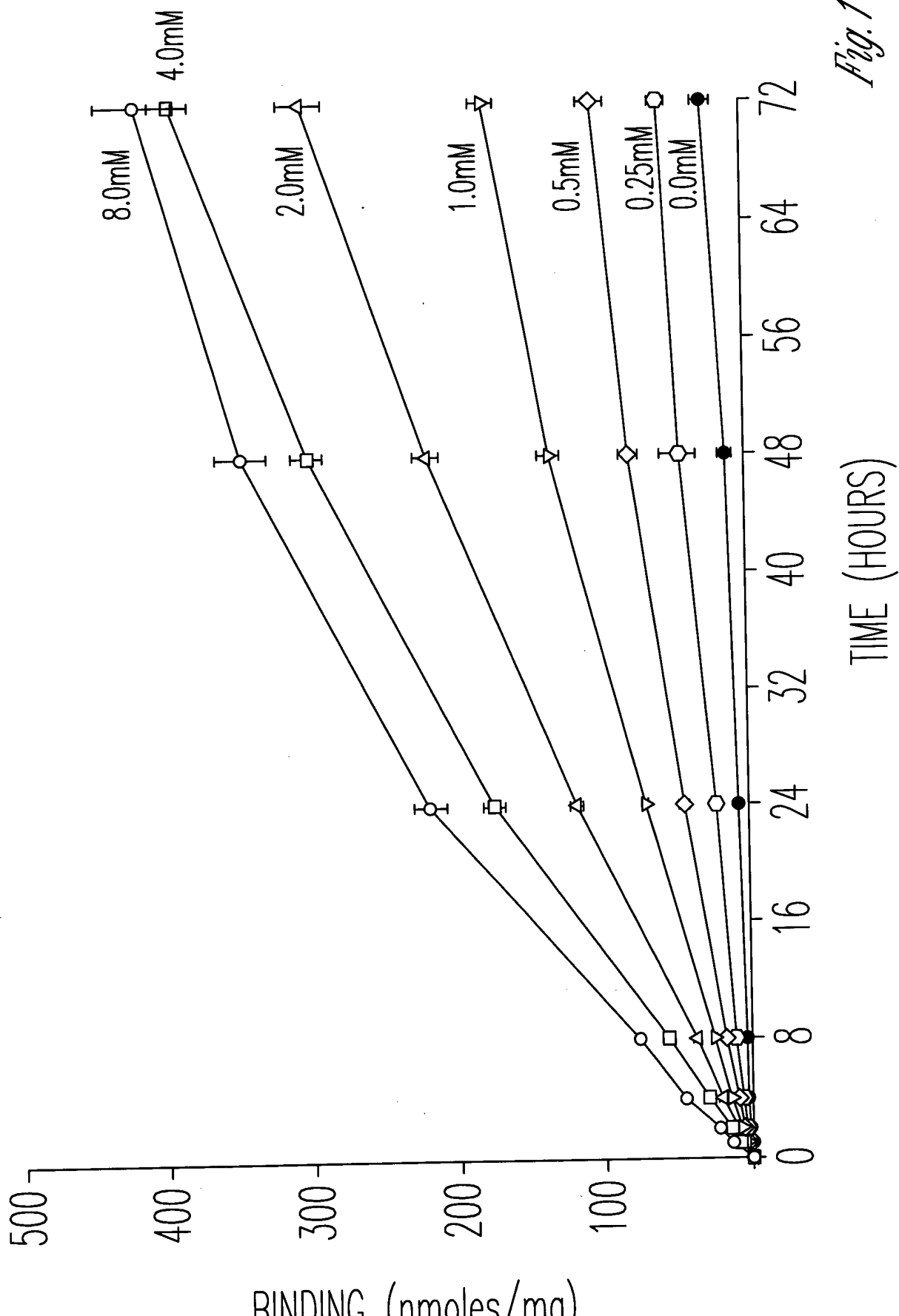
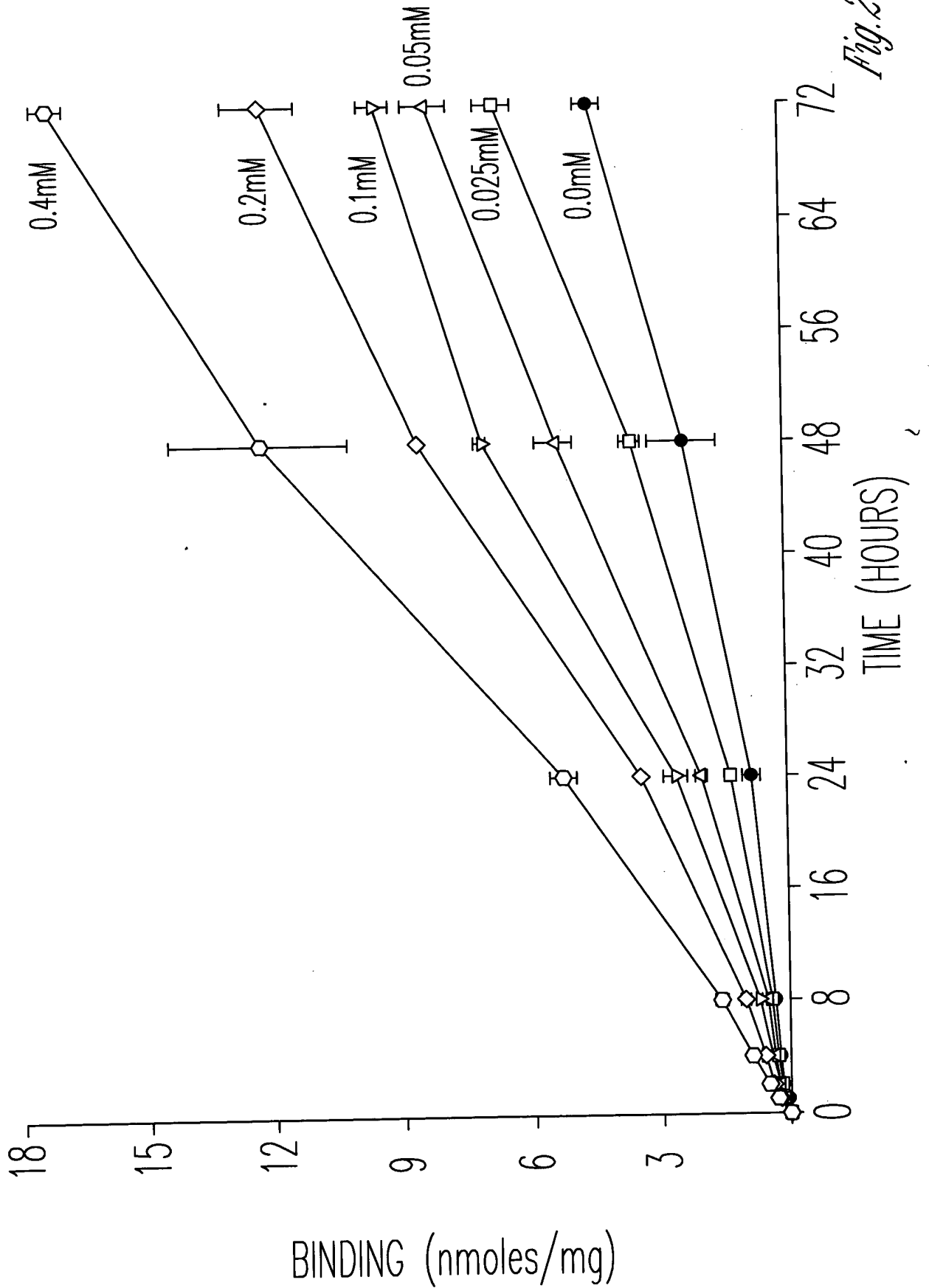


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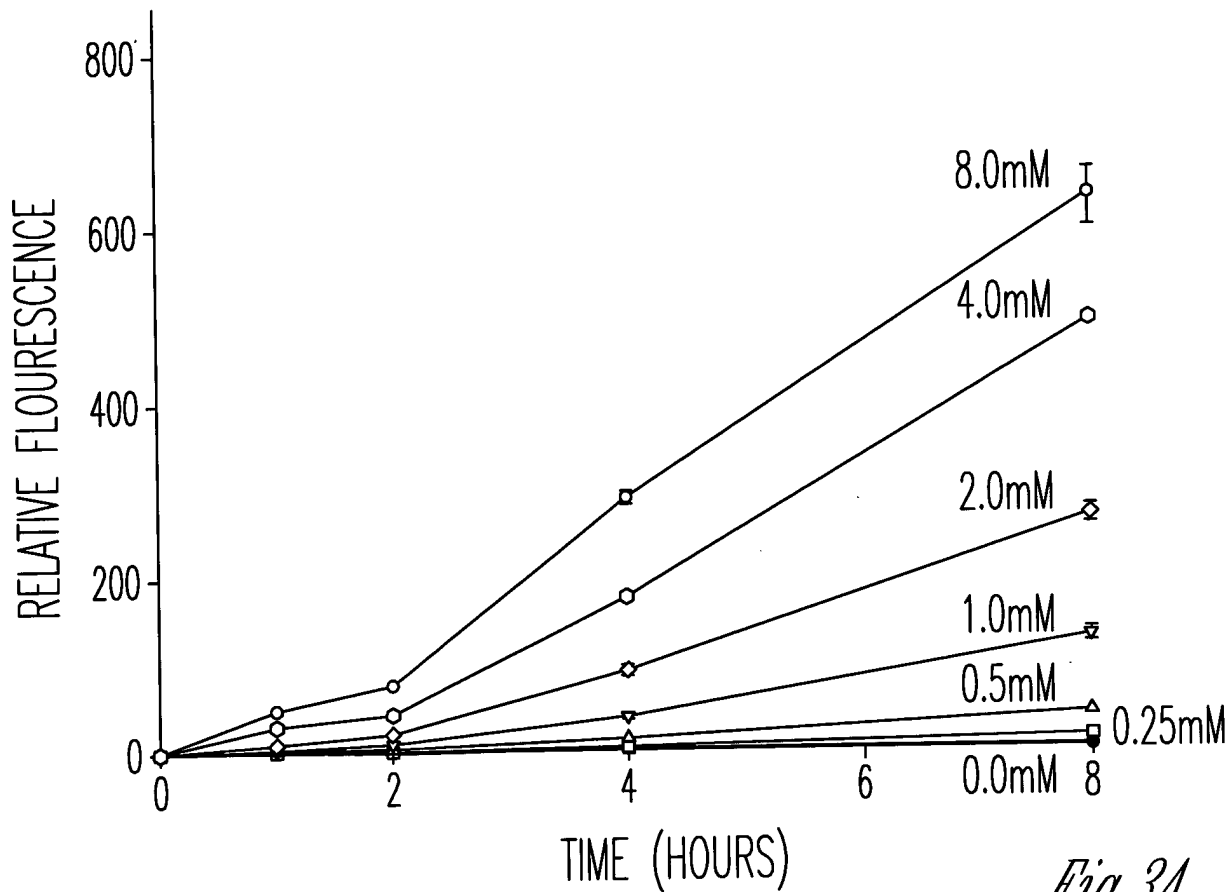


Fig. 3A

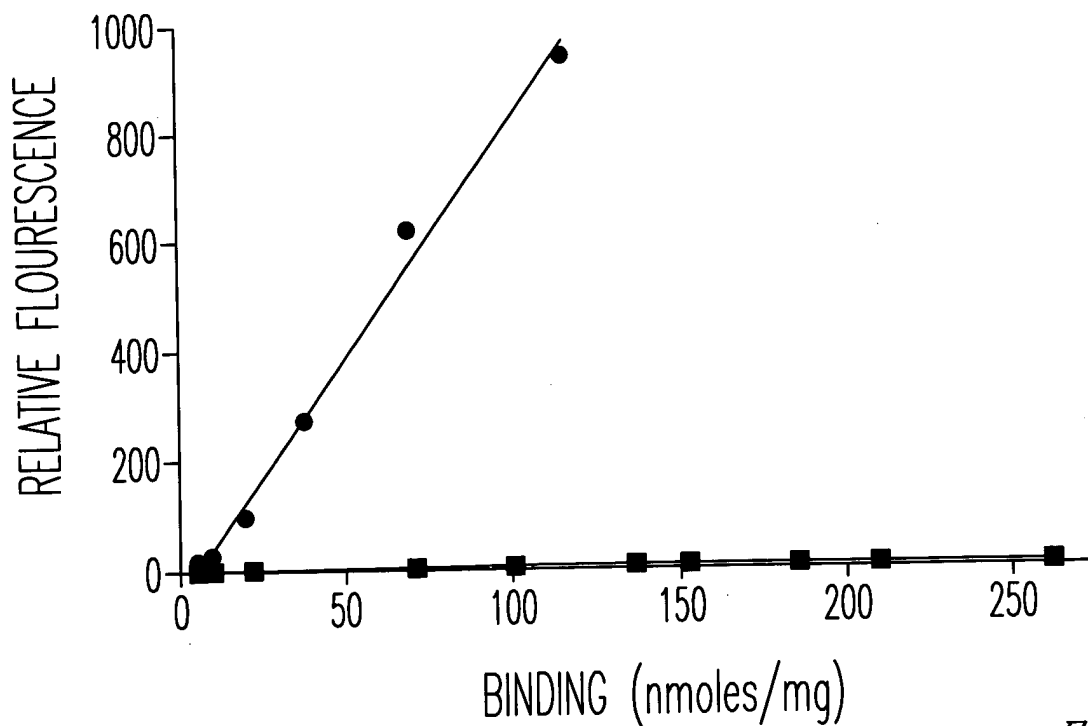


Fig. 3B

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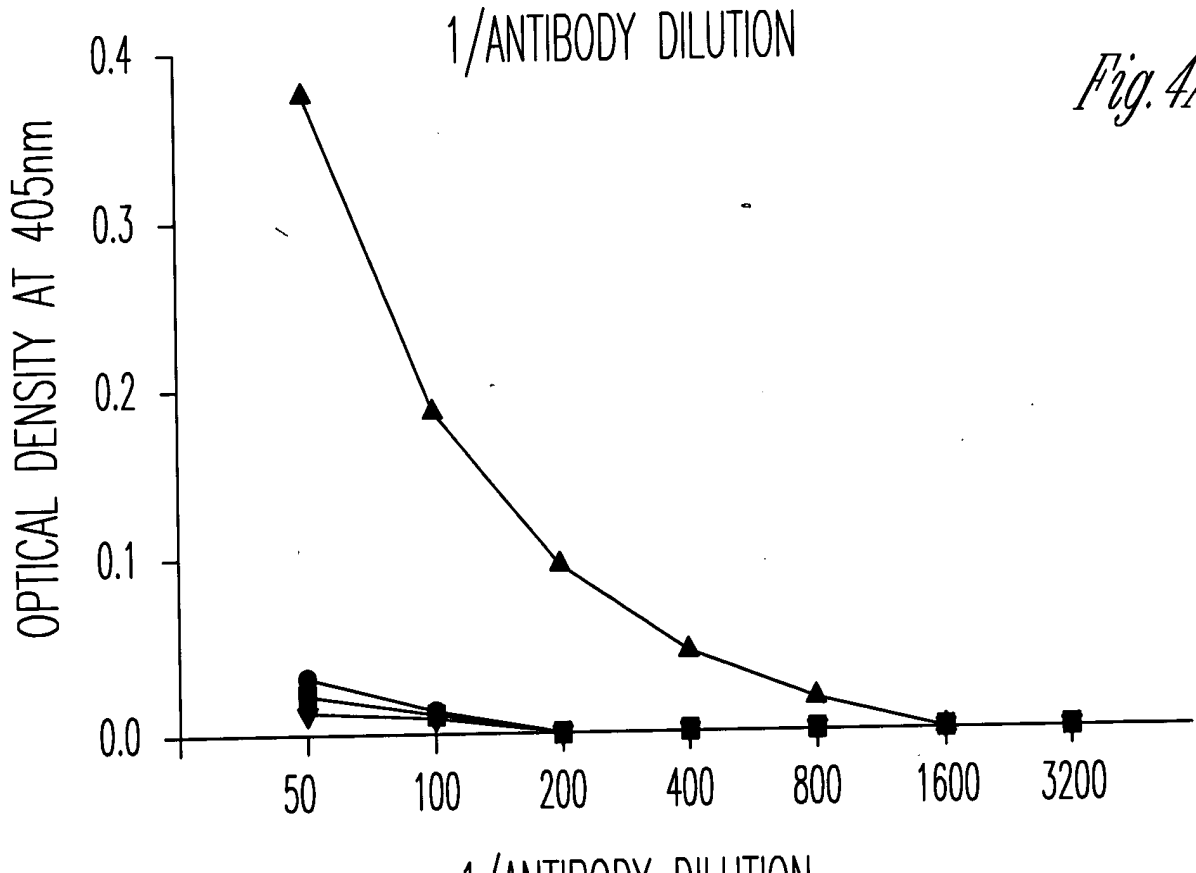
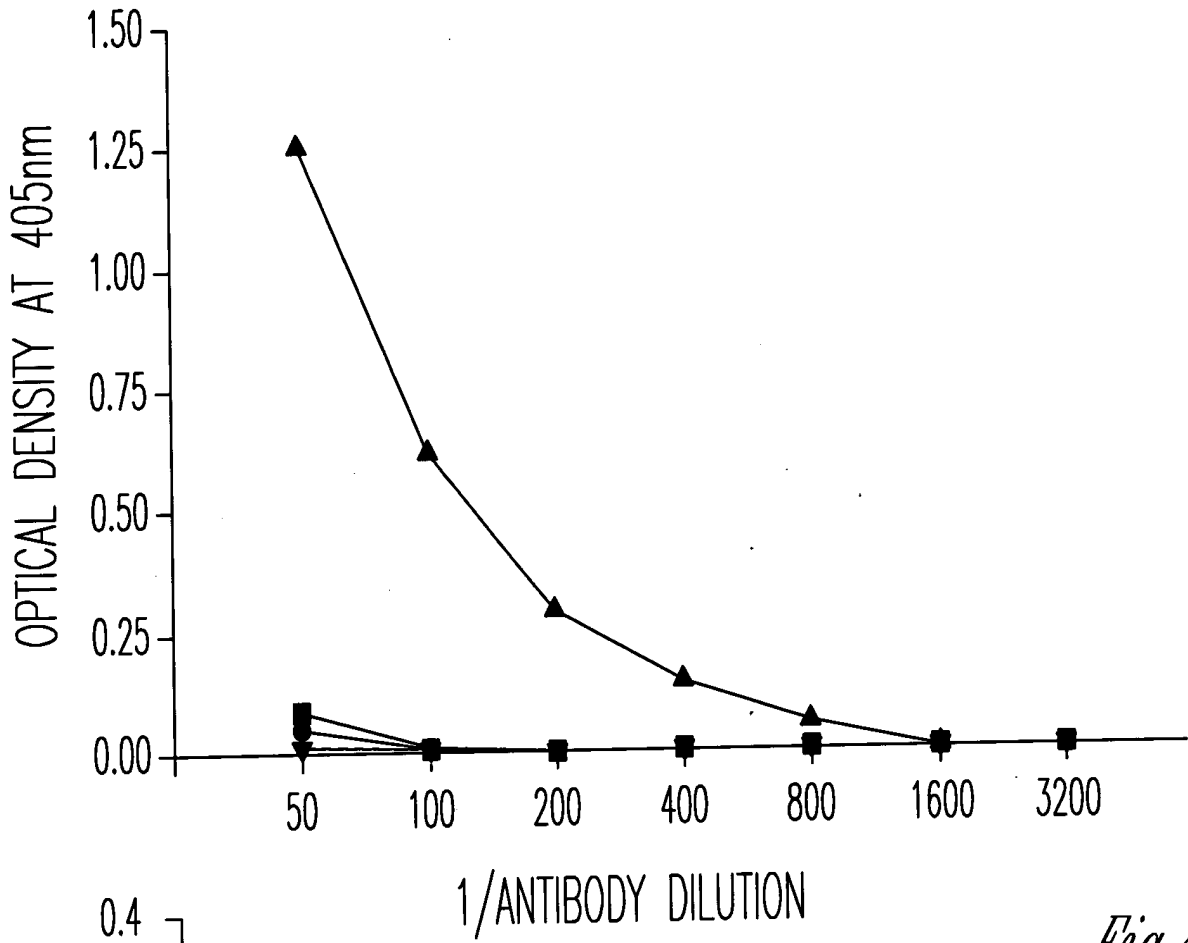
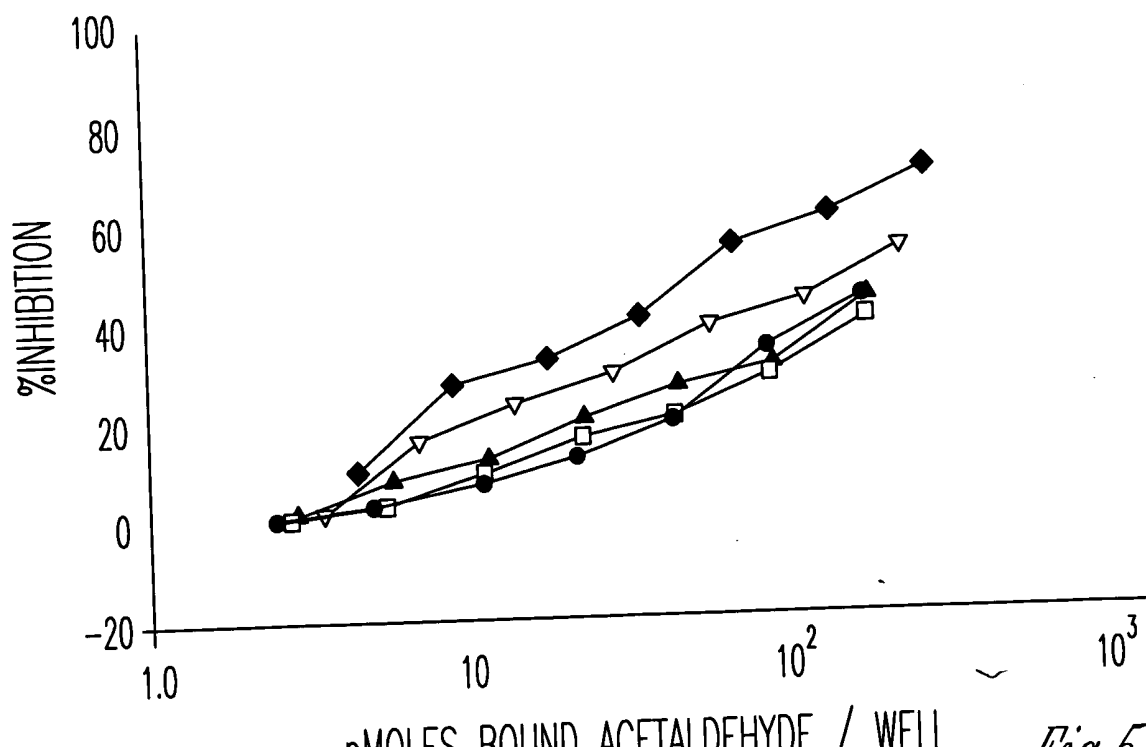
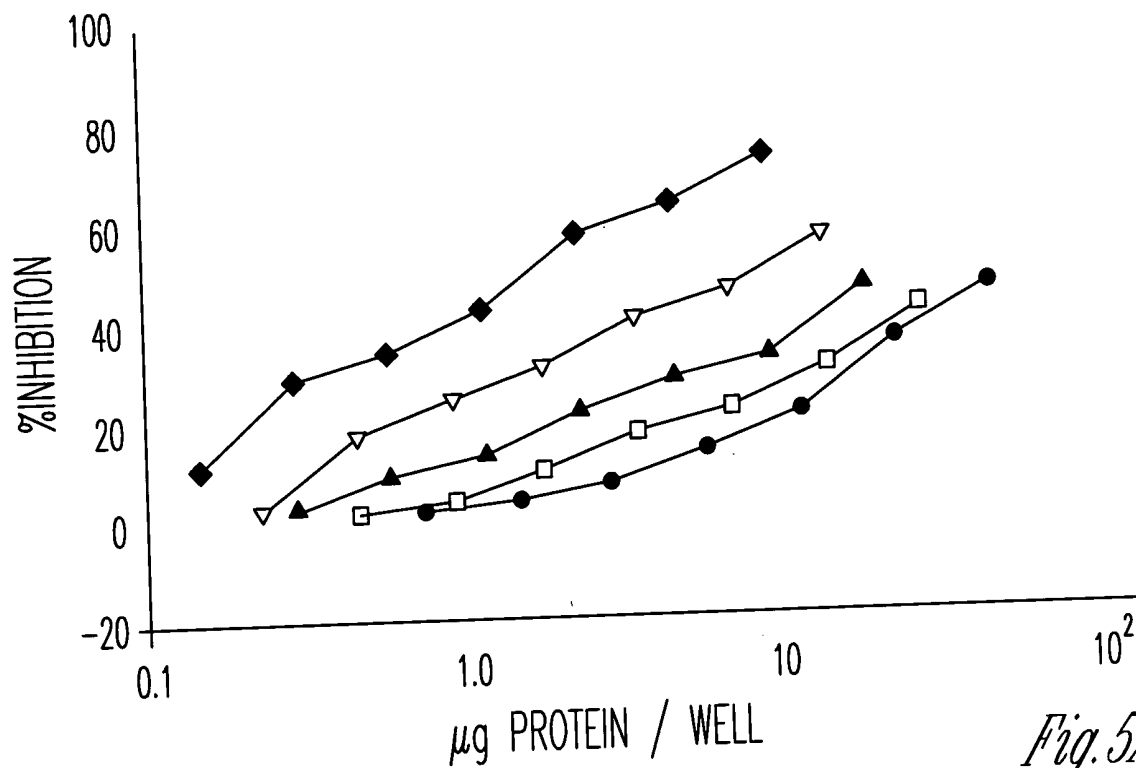
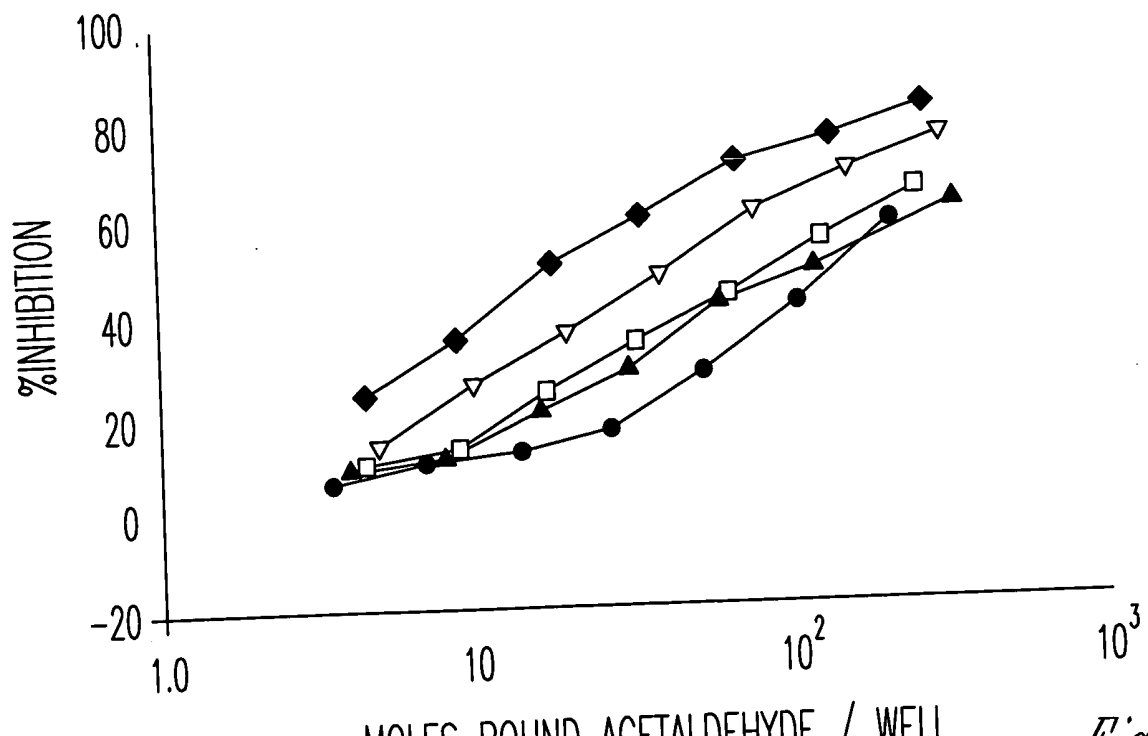
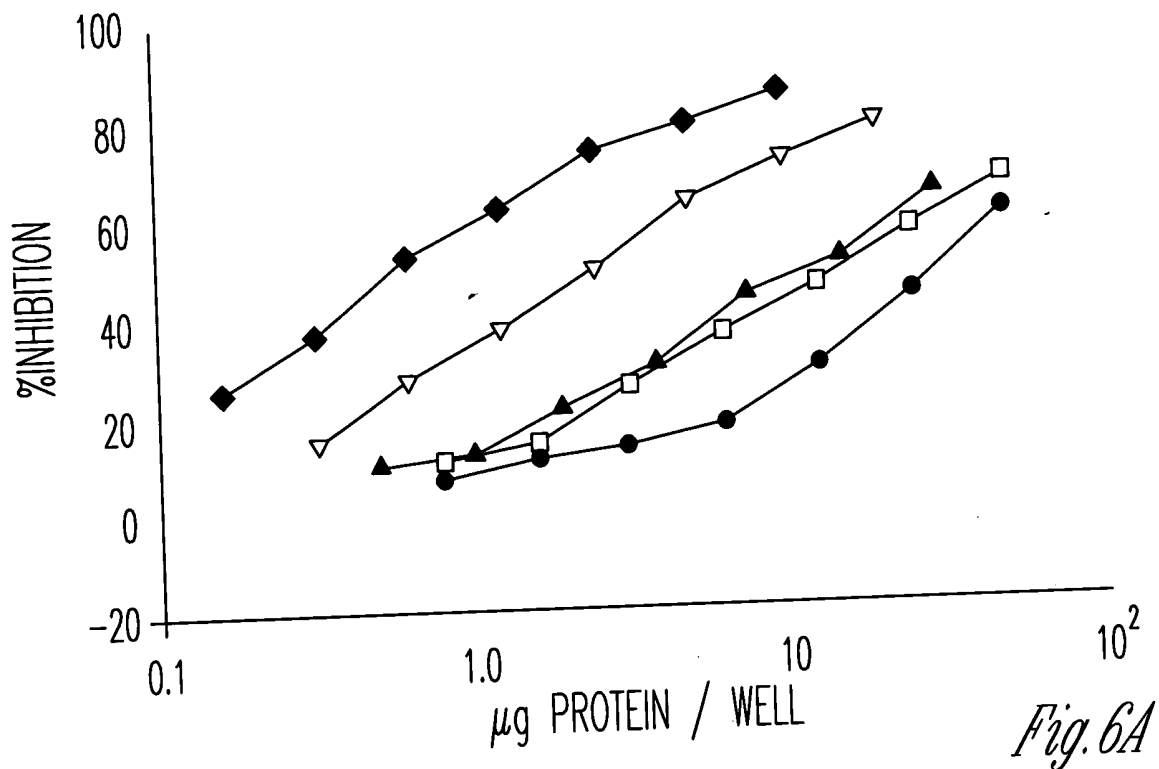


Fig. 4A

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[illegible]

Figure 7A is a line graph showing the percentage inhibition of various proteins as a function of protein concentration (μg protein / well) on a semi-logarithmic scale. The x-axis ranges from 10 to 10³ μg protein / well, and the y-axis ranges from -20 to 100% inhibition. Six data series are plotted, all showing a positive correlation between protein concentration and inhibition percentage.

Protein Concentration (μg / well)	Series 1 (Open Hexagon)	Series 2 (Solid Circle)	Series 3 (Open Square)	Series 4 (Solid Diamond)	Series 5 (Solid Triangle)	Series 6 (Open Inverted Triangle)
~15	23	13	6	3	2	0
~30	38	35	18	12	10	8
~60	50	44	28	24	19	13
~120	63	55	38	35	27	19
~250	71	66	48	46	39	26
~500	82	76	61	59	54	44
~1000	93	87	79	78	71	62

Figure 2B is a semi-logarithmic plot showing the percentage inhibition of ^{125}I -anti-IL-2 binding by various compounds. The y-axis represents '%INHIBITION' from -20 to 100. The x-axis represents 'pMOLES BOUND ACETALDEHYDE / WELL' on a logarithmic scale from 1.0 to 10^4 . Six curves are shown, each with a different marker: open circles, filled circles, open squares, filled triangles, open inverted triangles, and filled diamonds. All curves show a sigmoidal increase in inhibition as the concentration of bound acetaldehyde increases.

pMOLES BOUND ACETALDEHYDE / WELL	%INHIBITION (Open Circles)	%INHIBITION (Filled Circles)	%INHIBITION (Open Squares)	%INHIBITION (Filled Triangles)	%INHIBITION (Open Inverted Triangles)	%INHIBITION (Filled Diamonds)
10	10	10	10	10	10	10
100	50	45	40	35	30	25
1000	90	85	75	70	60	55

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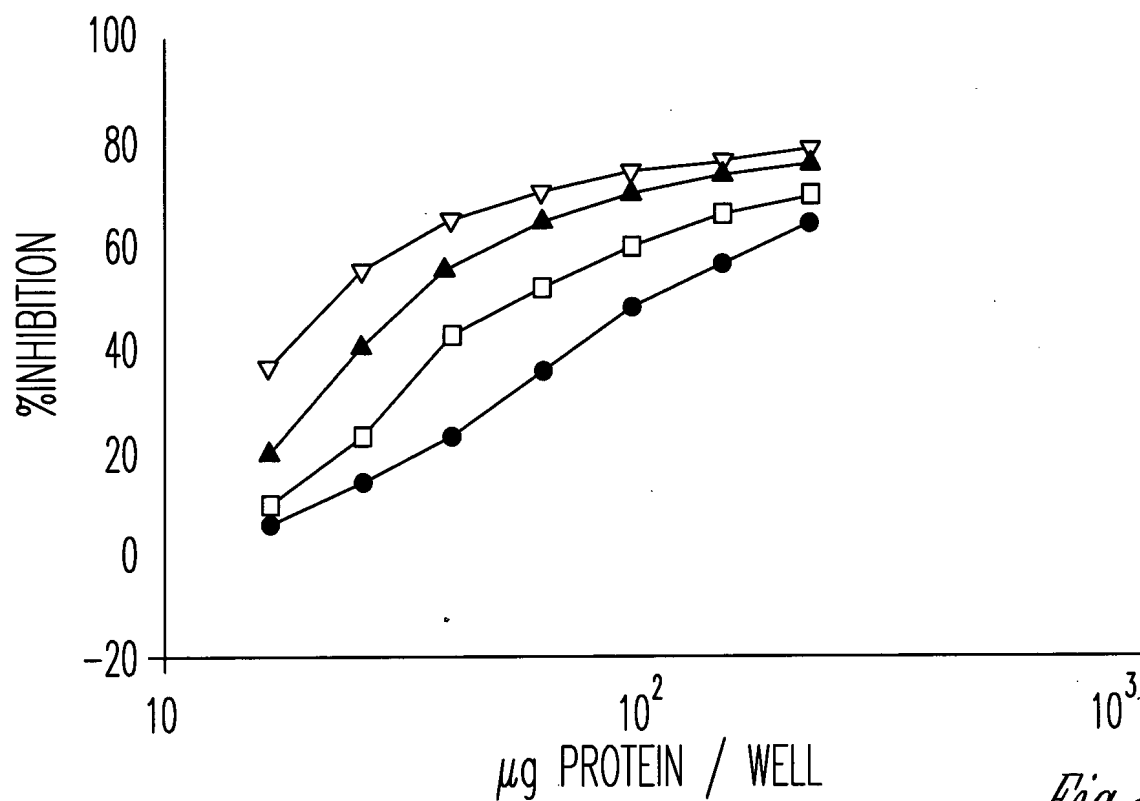


Fig. 8A

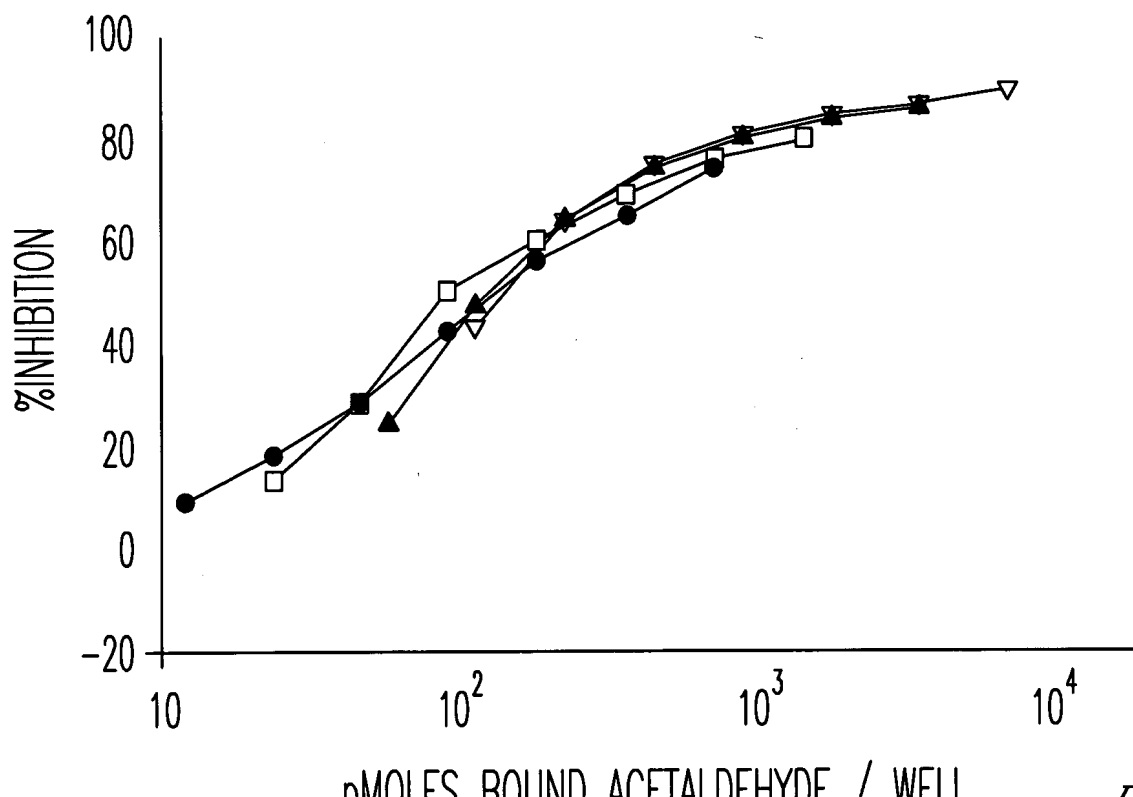


Fig. 8B

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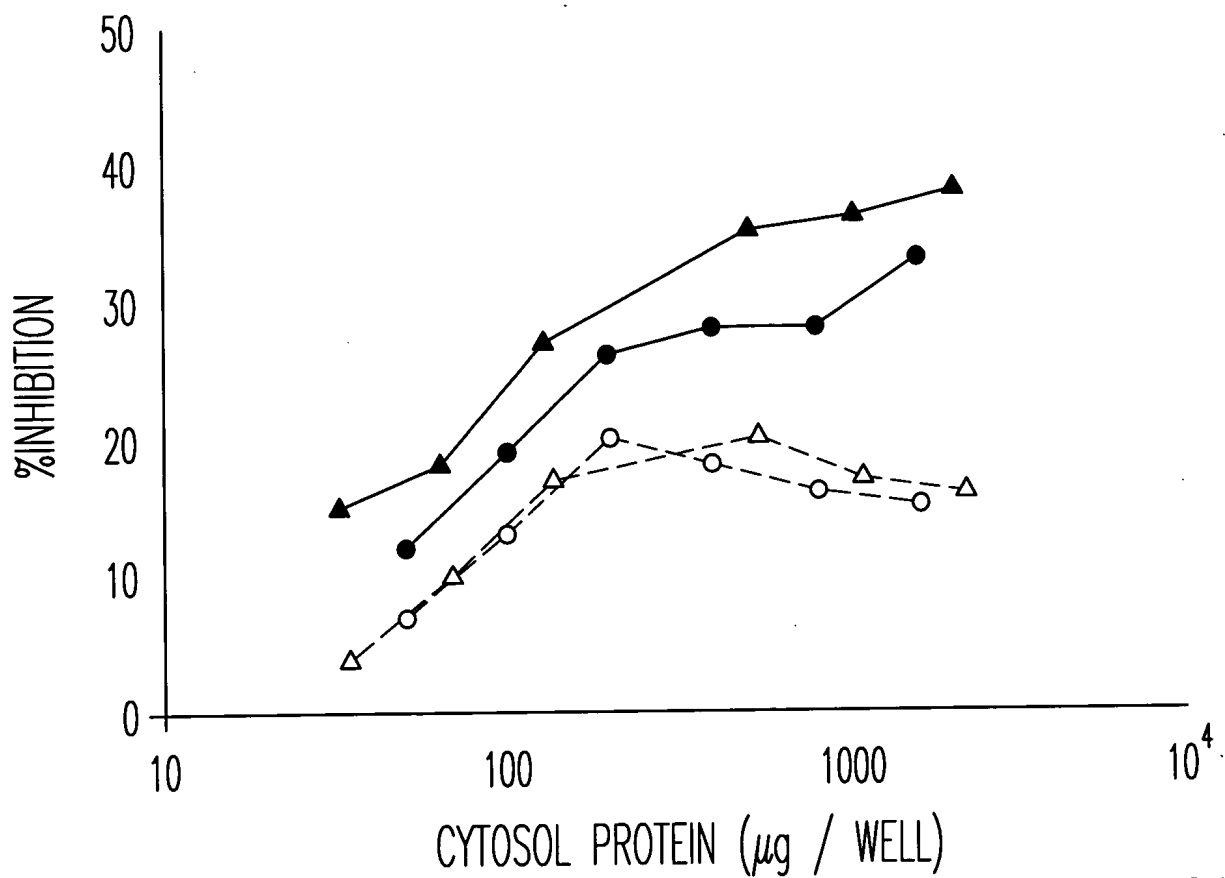


Fig. 9A

